RAW SEQUENCE LISTING
PATENT APPLICATION: **US/09/502,498B**

DATE: 10/10/2003
TIME: 10:59:17

Input Set : **A:\sequence listing 407C2.txt**
Output Set: **N:\CRF4\10102003\I502498B.raw**

P.6

ENTERED

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 3 <110> APPLICANT: Kilian, Andrzej
 4        Bowtell, David
 6 <120> TITLE OF INVENTION: VERTEBRATE TELOMERASE GENES AND PROTEINS AND USES
 7        THEREOF
 9 <130> FILE REFERENCE: 407C2
11 <140> CURRENT APPLICATION NUMBER: 09/502,498B
12 <141> CURRENT FILING DATE: 2000-02-11
14 <160> NUMBER OF SEQ ID NOS: 155
16 <170> SOFTWARE: PatentIn Ver. 2.0
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 3964
20 <212> TYPE: DNA
21 <213> ORGANISM: Homo sapiens
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25 gtgctgccgc tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctggtgcag 120
26 cgcggggacc cggcggcttt ccgcgcgctg gtggcccagt gcctggtgtg cgtgccctgg 180
27 gacgcacggc cgccccccgc cgccccctcc ttccgccagg tgtcctgcct gaaggagctg 240
28 gtggcccgag tgctgcagag gctgtgcgag cgcggcgcga agaacgtgct ggccttcggc 300
29 ttcgcgctgc tggacggggc ccgcgggggc cccccccgagg ccttcaccac cagcgtgcgc 360
30 agctacctgc ccaacacggt gaccgacgca ctgcggggga gcggggcgtg ggggctgctg 420
31 ttgcgccgcg tgggcgacga cgtgctggtt cacctgctgg cacgctgcgc gctctttgtg 480
32 ctggtggctc ccagctgcgc ctaccaggtg tgcgggccgc cgctgtacca gctcggcgct 540
33 gccactcagg cccggccccc gccacacgct agtggacccc gaaggcgtct gggatgcgaa 600
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35 gcgaggaggc gcggggggcag tgccagccga agtctgccgt tgcccaagag gcccaggcgt 720
36 ggcgctgccc ctgagccgga gcggacgccc gttgggcagg ggtcctgggc ccaccgggc 780
37 aggacgcgtg accgagtga ccgtggtttc tgtgtggtgt cacctgccag acccgccgaa 840
38 gaagccacct ctttggaggg tgcgctctct ggcacgcgcc actcccaccc atccgtgggc 900
39 cgccagcacc acgcgggccc cccatccaca tcgcggccac cacgtccctg ggacacgcct 960
40 tgtcccccgg tgtacgccga gaccaagcac ttcctctact cctcaggcga caaggagcag 1020
41 ctgcggccct ccttcctact cagctctctg aggcccagcc tgactggcgc tcggaggctc 1080
42 gtggagacca tctttctggg ttccaggccc tggatgccag ggactccccg caggttgccc 1140
43 cgcctgcccc agcgctactg gcaaatgcgg cccctgtttc tggagctgct tgggaaccac 1200
44 gcgcagtgcc cctacggggt gctcctcaag acgcactgcc cgctgcgagc tgcggtcacc 1260
45 ccagcagccg gtgtctgtgc ccgggagaag ccccagggct ctgtggcggc ccccgaggag 1320
46 gaggacacag acccccgtcg cctggtgcag ctgctccgcc agcacagcag cccctggcag 1380
47 gtgtacggct tcgtgcgggc ctgcctgcgc cggctggtgc ccccaggcct ctggggctcc 1440
48 aggcacaacg aacgccgctt cctcaggaac accaagaagt tcatctccct ggggaagcat 1500
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50 cgcaggagcc caggggttgg ctgtgttccg gccgcagagc accgtctgcg tgaggagatc 1620
51 ctggccaagt tcctgcactg gctgatgagt gtgtacgtcg tcgagctgct caggtctttc 1680
52 ttttatgtca cggagaccac gtttcaaaag aacaggctct ttttctaccg gaagagtgtc 1740
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53 tggagcaagt tgcaaagcat tggaatcaga cagcacttga agagggtgca gctgcgggag 1800
54 ctgtcggaag cagaggtcag gcagcatcgg gaagccaggc ccgccctgct gacgtccaga 1860
55 ctccgcttca tccccaagcc tgacgggctg cggccgattg tgaacatgga ctacgtcgtg 1920
56 ggagccagaa cgttccgcag agaaaagagg gccgagcgtc tcacctcgag ggtgaaggca 1980
57 ctgttcagcg tgctcaacta cgagcgggcg cggcgccccg gcctcctggg cgcctctgtg 2040
58 ctgggcctgg acgatatcca cagggcctgg cgcaccttcg tgctgcgtgt gcgggcccag 2100
59 gacccgccgc ctgagctgta ctttgtcaag gtggatgtga cgggcgcgta cgacaccatc 2160
60 ccccaggaca ggctcacgga ggtcatcgcc agcatcatca aaccccagaa cacgtactgc 2220
61 gtgcgtcggt atgccgtggt ccagaaggcc gcccatgggc acgtccgcaa ggccttcaag 2280
62 agccacgtct ctaccttgac agacctccag ccgtacatgc gacagttcgt ggctcacctg 2340
63 caggagacca gcccgctgag ggatgccgtc gtcatcgagc agagctcctc cctgaatgag 2400
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65 aggggcaagt cctacgtcca gtgccagggg atcccgcagg gctccatcct ctccacgctg 2520
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69 cggaagacag tggtgaactt ccctgtagaa gacgaggccc tgggtggcac ggctttttgtt 2760
70 cagatgccgg cccacggcct attcccctgg tgcggcctgc tgctggatac ccggaccctg 2820
71 gaggtgcaga gcgactactc cagctatgcc cggacctcca tcagagccag tctcaccttc 2880
72 aaccgcggct tcaaggctgg gaggaacatg cgtcgcaaac tctttggggt cttgcggctg 2940
73 aagtgtcaca gcctgtttct ggatttgcag gtgaacagcc tccagacggt gtgcaccaac 3000
74 atctacaaga tcctcctgct gcaggcgtac aggtttcacg catgtgtgct gcagctccca 3060
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83 gcctgcatgt ccggctgaag gctgagtgtc cggctgaggc ctgagcgagt gtccagccaa 3600
84 gggctgagtg tccagcacac ctgccgtctt cacttcccca caggctggcg ctcggctcca 3660
85 ccccagggcc agcttttcct caccaggagc ccggcttcca ctccccacat aggaatagtc 3720
86 catcccaga ttcgccattg ttcacccctc gccctgccct cctttgcctt ccaccccac 3780
87 catccaggtg gagaccctga gaaggaccct gggagctctg ggaatttgga gtgaccaaag 3840
88 gtgtgccctg tacacaggcg aggaccctgc acctggatgg gggtccctgt gggtcaaatt 3900
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92 <210> SEQ ID NO: 2
93 <211> LENGTH: 1132
94 <212> TYPE: PRT
95 <213> ORGANISM: Homo sapiens
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99  1               5                  10                  15
101 His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
102             20                  25                  30
104 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
105             35                  40                  45
```

```
107 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
108         50              55              60
110 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
111  65              70              75                          80
113 Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
114             85              90                          95
116 Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
117             100             105             110
119 Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
120         115             120                 125
122 Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
123         130             135             140
125 Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
126 145             150             155                         160
128 Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
129             165             170             175
131 Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
132             180             185             190
134 Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
135         195             200             205
137 Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
138         210             215             220
140 Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
141 225             230             235                         240
143 Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
144             245             250             255
146 Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
147             260             265             270
149 Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
150         275             280             285
152 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
153         290             295             300
155 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
156 305             310             315             320
158 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
159             325             330             335
161 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
162         340             345             350
164 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
165         355             360             365
167 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
168         370             375             380
170 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
171 385             390             395                         400
173 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
174             405             410             415
176 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
177             420             425             430
179 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
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180         435                440                445
182 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
183     450                455                460
185 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
186 465                470                475                480
188 Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
189                 485                490                495
191 Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
192             500                505                510
194 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
195         515                520                525
197 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
198     530                535                540
200 Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
201 545                550                555                560
203 Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
204             565                570                575
206 Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
207         580                585                590
209 Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
210         595                600                605
212 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
213     610                615                620
215 Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
216 625                630                635                640
218 Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
219             645                650                655
221 Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
222         660                665                670
224 Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
225         675                680                685
227 Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
228     690                695                700
230 Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile
231 705                710                715                720
233 Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln
234             725                730                735
236 Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His
237             740                745                750
239 Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp
240         755                760                765
242 Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser
243     770                775                780
245 Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu
246 785                790                795                800
248 Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His
249             805                810                815
251 Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro
252         820                825                830
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```
254 Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp
255         835             840             845
257 Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu
258     850             855             860
260 Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala
261 865             870             875             880
263 Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys
264             885             890             895
266 Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu
267         900             905             910
269 Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe
270         915             920             925
272 Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser
273     930             935             940
275 Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe
276 945             950             955             960
278 Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly
279             965             970             975
281 Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn
282         980             985             990
284 Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln
285         995             1000            1005
287 Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln
288     1010            1015            1020
290 Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala
291 1025            1030            1035            1040
293 Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu
294             1045            1050            1055
296 Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp
297             1060            1065            1070
299 Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr
300         1075            1080            1085
302 Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser
303     1090            1095            1100
305 Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn
306 1105            1110            1115            1120
308 Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
309             1125            1130
312 <210> SEQ ID NO: 3
313 <211> LENGTH: 1031
314 <212> TYPE: PRT
315 <213> ORGANISM: Euplotes aediculatus
317 <400> SEQUENCE: 3
318 Met Glu Val Asp Val Asp Asn Gln Ala Asp Asn His Gly Ile His Ser
319   1             5               10              15
321 Ala Leu Lys Thr Cys Glu Glu Ile Lys Glu Ala Lys Thr Leu Tyr Ser
322             20              25              30
324 Trp Ile Gln Lys Val Ile Arg Cys Arg Asn Gln Ser Gln Ser His Tyr
325         35              40              45
```

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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:15; N Pos. 1,2,3,4,5,6,7
Seq#:34; N Pos. 1767,1768,1769
Seq#:51; N Pos. 1871,1872,1873
Seq#:91; Xaa Pos. 2,3,4,5
Seq#:93; Xaa Pos. 2,3,4,5,7,8
Seq#:95; N Pos. 1,2,3,5,9,10,11,12,13,14

VERIFICATION SUMMARY   DATE: 10/10/2003
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```
L:1039 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0
L:1356 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34 after pos.:1740
L:3364 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51 after pos.:1860
L:9327 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:91 after pos.:0
L:9364 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:93 after pos.:0
L:9406 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:95 after pos.:0
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